What is Claimed is:

1. A method for haplotyping the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) gene of an individual, which comprises determining which of the TNFRSF11B haplotypes shown in the table immediately below defines one copy of the individual's TNFRSF11B gene, wherein the determining step comprises identifying the phased sequence of nucleotides present at each of PS1-PS19 on at least one copy of the individual's TNFRSF11B gene, and wherein each of the TNFRSF11B haplotypes comprises a sequence of polymorphisms whose positions and identities are set forth in the table immediately below:

PS	PS	Haplotype Number(c) (Part 1)									
No.(a)	Position(b)	1	2	3	4	5	6	7	8	9	10
1	504	G	G	G	G	G	G	G	G	G	G
2	717	C	C	C	C	C	C	C	C	C	C
3	744	G	G	G	G	G	G	G	G	G	G
4	778	C	C	C	C	C	C	C	T	T	T
5	1009	C	C	G	G	G	G	G	C	C	C
6	1045	C	C	T	T	T	T	T	C	C	C
7	1122	G	G	A	G	G	G	G	G	G	G
8	1218	C	C	C	C	C	C	C	A	A	C
9	2014	C	C	C	C	C	C	T	C	C	C
10	2177	T	T	T	T	T	T	C	T	T	T
11	5906	C	T	T	C	T	T	T	C	T	C
12	6010	C	C	C	C	C	T	T	C	C	C
13	8110	G	G	G	G	G	G	G	G	G	G
14	8333	C	C	C	C	C	C	T	C	C	C
15	8354	A	A	A	A	A	A	A	G	A	A
16	8402	A	A	A	A	A	A	G	A	A	A
17	8459	A	A	A	A	A	A	A	A	A	A
18	10203	G	G	G	G	G	G	G	G	G	G
19	10512	T	T	C	T	T	T	T	T	T	T

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PS No.(a)	PS Position(b)	Haplotype Number(c) (Part 2) 11	12	13	14	15	16	17	18	19	20
1	504	G	G	G	G	G	G	G	G	G	G
2	717	C	C	C	C	C	C	C	C	C	C
3	744	G	G	G	G	G	G	G	G	G	T
4	778	T	T	T	T	T	T	T	T	T	T
5	1009	C	C	G	G	G	G	G	G	G	G
6	1045	C	C	C	C	C	C	C	C	C	C
7	1122	G	G	G	G	G	G	G	G	G	G
8	1218	C	C	A	A	A	C	C	C	C	C
9	2014	C	T	C	C	C	C	C	C	C	C
10	2177	T	C	T	T	T	T	T	T	T	T
11	5906	T	T	C	T	T	C	T	T	T	T
12	6010	C	C	C	C	C	C	C	C	C	C
13	8110	G	G	A	G	G	G	A	G	G	G
14	8333	C	C	C	C	C	C	C	C	C	C
15	8354	A	A	A	A	A	A	A	A	A	A
16	8402	A	G	A	A	A	A	A	A	A	A
17	8459	A	C	A	A	A	A	A	A	A	A
18	10203	A	G	G	G	G	G	G	G	G	G
19	10512	T	T	C	C	T	T	T	C	T	T

PS No.(a)	PS Position(b)	Haplotype Number(c) (Part 3) 21	22
1	504	G	T
2	717	T	C
3	744	G	G
4	778	C	T
5	1009	C	G
6	1045	C	C
7	1122	G	G
8	1218	C	C
9	2014	C	C
10	2177	T	T
11	5906	C	T
12	6010	C	C
13	8110	G	A
14	8333	C	C
15	8354	A	A
16	8402	A	A
17	8459	A	A
18	10203	G	G
19	10512	T	C

(a) PS = polymorphic site;
(b) Position of PS within SEQ ID NO:1;
(c) Alleles for haplotypes are presented 5′ to 3′ in each column.

2. A method for haplotyping the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) gene of an individual, which comprises determining which of the TNFRSF11B haplotype pairs shown in the table immediately below defines both copies of the individual's TNFRSF11B gene, wherein the determining step comprises identifying the phased sequence of nucleotides present at each of PS1-PS19 on both copies of the individual's TNFRSF11B gene, and wherein each of the TNFRSF11B haplotype pairs consists of first and second haplotypes which comprise first and second sequences of polymorphisms whose positions and identities are set forth in the table immediately below:

PS No.(a)	PS Position(b)	Haplotype Pair(c) (Part 1) 1/1	15/15	19/19	6/6	12/12	19/16	10/2	1/5
1	504	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
2	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
4	778	C/C	T/T	T/T	C/C	T/T	T/T	T/C	C/C
5	1009	C/C	G/G	G/G	G/G	C/C	G/G	C/C	C/G
6	1045	C/C	C/C	C/C	T/T	C/C	C/C	C/C	C/T
7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
8	1218	C/C	A/A	C/C	C/C	C/C	C/C	C/C	C/C
9	2014	C/C	C/C	C/C	C/C	T/T	C/C	C/C	C/C
10	2177	T/T	T/T	T/T	T/T	C/C	T/T	T/T	T/T
11	5906	C/C	T/T	T/T	T/T	T/T	T/C	C/T	C/T
12	6010	C/C	C/C	C/C	T/T	C/C	C/C	C/C	C/C
13	8110	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
15	8354	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
16	8402	A/A	A/A	A/A	A/A	G/G	A/A	A/A	A/A
17	8459	A/A	A/A	A/A	A/A	C/C	A/A	A/A	A/A
18	10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
19	10512	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T

PS No.(a)	PS Position(b)	Haplotype Pair(c) (Part 2) 10/14	19/14	19/13	15/12	1/21	19/11	15/6	1/6
1	504	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
2	717	C/C	C/C	C/C	C/C	C/T	C/C	C/C	C/C
3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
4	778	T/T	T/T	T/T	T/T	C/C	T/T	T/C	C/C
5	1009	C/G	G/G	G/G	G/C	C/C	G/C	G/G	C/G
6	1045	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/T
7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
8	1218	C/A	C/A	C/A	A/C	C/C	C/C	A/C	C/C
9	2014	C/C	C/C	C/C	C/T	C/C	C/C	C/C	C/C
10	2177	T/T	T/T	T/T	T/C	T/T	T/T	T/T	T/T
11	5906	C/T	T/T	T/C	T/T	C/C	T/T	T/T	C/T
12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/T
13	8110	G/G	G/G	G/A	G/G	G/G	G/G	G/G	G/G
14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
15	8354	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
16	8402	A/A	A/A	A/A	A/G	A/A	A/A	A/A	A/A
17	8459	A/A	A/A	A/A	A/C	A/A	A/A	A/A	A/A
18	10203	G/G	G/G	G/G	G/G	G/G	G/A	G/G	G/G
19	10512	T/C	T/C	T/C	T/T	T/T	T/T	T/T	T/T

PS No.(a)	PS Position(b)	Haplotype Pair(c) (Part 3) 1/2	19/4	19/3	19/9	15/3	19/20	19/7	19/18
1	504	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
2	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
3	744	G/G	G/G	G/G	G/G	G/G	G/T	G/G	G/G
4	778	C/C	T/C	T/C	T/T	T/C	T/T	T/C	T/T
5	1009	C/C	G/G	G/G	G/C	G/G	G/G	G/G	G/G
6	1045	C/C	C/T	C/T	C/C	C/T	C/C	C/T	C/C
7	1122	G/G	G/G	G/A	G/G	G/A	G/G	G/G	G/G
8	1218	C/C	C/C	C/C	C/A	A/C	C/C	C/C	C/C
9	2014	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C
10	2177	T/T	T/T	T/T	T/T	T/T	T/T	T/C	T/T
11	5906	C/T	T/C	T/T	T/T	T/T	T/T	T/T	T/T
12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C
13	8110	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C
15	8354	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
16	8402	A/A	A/A	A/A	A/A	A/A	A/A	A/G	A/A
17	8459	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
18	10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
19	10512	T/T	T/T	T/C	T/T	T/C	T/T	T/T	T/C

PS No.(a)	PS Position(b)	Haplotype Pair(c) (Part 4) 22/17	19/12	1/12	19/8	15/10	19/15	19/10	18/16
1	504	T/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
2	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
4	778	T/T	T/T	C/T	T/T	T/T	T/T	T/T	T/T
5	1009	G/G	G/C	C/C	G/C	G/C	G/G	G/C	G/G
6	1045	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
8	1218	C/C	C/C	C/C	C/A	A/C	C/A	C/C	C/C
9	2014	C/C	C/T	C/T	C/C	C/C	C/C	C/C	C/C
10	2177	T/T	T/C	T/C	T/T	T/T	T/T	T/T	T/T
11	5906	T/T	T/T	C/T	T/C	T/C	T/T	T/C	T/C
12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
13	8110	A/A	G/G	G/G	G/G	G/G	G/G	G/G	G/G
14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
15	8354	A/A	A/A	A/A	A/G	A/A	A/A	A/A	A/A
16	8402	A/A	A/G	A/G	A/A	A/A	A/A	A/A	A/A
17	8459	A/A	A/C	A/C	A/A	A/A	A/A	A/A	A/A
18	10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
19	10512	C/T	T/T	T/T	T/T	T/T	T/T	T/T	C/T

PS No.(a)	PS Position(b)	Haplotype Pair(c) (Part 5) 3/14
1	504	G/G
2	717	C/C
3	744	G/G
4	778	C/T
5	1009	G/G
6	1045	T/C
7	1122	A/G
8	1218	C/A
9	2014	C/C
10	2177	T/T
11	5906	T/T
12	6010	C/C
13	8110	G/G
14	8333	C/C
15	8354	A/A
16	8402	A/A
17	8459	A/A
18	10203	G/G
19	10512	C/C

(a) PS = polymorphic site;
(b) Position of PS in SEQ ID NO:1;
(c) Haplotype pairs are represented as 1st haplotype/2nd haplotype; with alleles of each haplotype shown 5′ to 3′ as 1st polymorphism/2nd polymorphism in each column.

3. A method for genotyping the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) gene of an individual, comprising determining for the two copies of the TNFRSF11B gene present in the individual the identity of the nucleotide pair at one or more polymorphic sites (PS) selected from the group consisting of PS1, PS2, PS3, PS4, PS6, PS7, PS8, PS9, PS10, PS11, PS12, PS13, PS14, PS15, PS16, PS17, PS18 and PS19, wherein the one or more polymorphic sites (PS) have the position and alternative alleles shown in SEQ ID NO:1.

4. The method of claim 3, wherein the determining step comprises:

   (a) isolating from the individual a nucleic acid mixture comprising both copies of the TNFRSF11B gene, or a fragment thereof, that are present in the individual;

   (b) amplifying from the nucleic acid mixture a target region containing one of the selected polymorphic sites;

   (c) hybridizing a primer extension oligonucleotide to one allele of the amplified target region, wherein the oligonucleotide is designed for genotyping the selected polymorphic site in the target region;

   (d) performing a nucleic acid template-dependent, primer extension reaction on the hybridized oligonucleotide in the presence of at least one terminator of the reaction, wherein the terminator is complementary to one of the alternative nucleotides present at the selected polymorphic site; and

   (e) detecting the presence and identity of the terminator in the extended oligonucleotide.

5. The method of claim 3, which comprises determining for the two copies of the TNFRSF11B gene present in the individual the identity of the nucleotide pair at each of PS1-PS19.

6. A method for haplotyping the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) gene of an individual which comprises determining, for one copy of the TNFRSF11B gene present in the individual, the identity of the nucleotide at two or more polymorphic sites (PS) selected from the group consisting of PS1, PS2, PS3, PS4, PS6, PS7, PS8, PS9, PS10, PS11, PS12, PS13, PS14, PS15, PS16, PS17, PS18 and PS19, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1.

7. The method of claim 6, further comprising determining the identity of the nucleotide at PS5, wherein the PS has the position and alternative alleles shown in SEQ ID NO:1.

8. The method of claim 6, wherein the determining step comprises:

   (a) isolating from the individual a nucleic acid sample containing only one of the two copies of the TNFRSF11B gene, or a fragment thereof, that is present in the individual;

   (b) amplifying from the nucleic acid sample a target region containing one of the selected polymorphic sites;

   (c) hybridizing a primer extension oligonucleotide to one allele of the amplified target region, wherein the oligonucleotide is designed for haplotyping the selected polymorphic site in

the target region;

(d) performing a nucleic acid template-dependent, primer extension reaction on the hybridized oligonucleotide in the presence of at least one terminator of the reaction, wherein the terminator is complementary to one of the alternative nucleotides present at the selected polymorphic site; and

(e) detecting the presence and identity of the terminator in the extended oligonucleotide.

9. A method for predicting a haplotype pair for the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) gene of an individual comprising:

(a) identifying a TNFRSF11B genotype for the individual, wherein the genotype comprises the nucleotide pair at two or more polymorphic sites (PS) selected from the group consisting of PS1, PS2, PS3, PS4, PS6, PS7, PS8, PS9, PS10, PS11, PS12, PS13, PS14, PS15, PS16, PS17, PS18 and PS19, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1;

(b) comparing the genotype to the haplotype pair data set forth in the table immediately below; and

(c) determining which haplotype pair is consistent with the genotype of the individual and with the haplotype pair data

PS No.(a)	PS Position(b)	Haplotype Pair(c) (Part 1) 1/1	15/15	19/19	6/6	12/12	19/16	10/2	1/5
1	504	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
2	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
4	778	C/C	T/T	T/T	C/C	T/T	T/T	T/C	C/C
5	1009	C/C	G/G	G/G	G/G	C/C	G/G	C/C	C/G
6	1045	C/C	C/C	C/C	T/T	C/C	C/C	C/C	C/T
7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
8	1218	C/C	A/A	C/C	C/C	C/C	C/C	C/C	C/C
9	2014	C/C	C/C	C/C	C/C	T/T	C/C	C/C	C/C
10	2177	T/T	T/T	T/T	T/T	C/C	T/T	T/T	T/T
11	5906	C/C	T/T	T/T	T/T	T/T	T/C	C/T	C/T
12	6010	C/C	C/C	C/C	T/T	C/C	C/C	C/C	C/C
13	8110	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
15	8354	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
16	8402	A/A	A/A	A/A	A/A	G/G	A/A	A/A	A/A
17	8459	A/A	A/A	A/A	A/A	C/C	A/A	A/A	A/A
18	10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
19	10512	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T

PS No.(a)	PS Position(b)	Haplotype Pair(c) (Part 2)							
		10/14	19/14	19/13	15/12	1/21	19/11	15/6	1/6
1	504	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
2	717	C/C	C/C	C/C	C/C	C/T	C/C	C/C	C/C
3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
4	778	T/T	T/T	T/T	T/T	C/C	T/T	T/C	C/C
5	1009	C/G	G/G	G/G	G/C	C/C	G/C	G/G	C/G
6	1045	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/T
7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
8	1218	C/A	C/A	C/A	A/C	C/C	C/C	A/C	C/C
9	2014	C/C	C/C	C/C	C/T	C/C	C/C	C/C	C/C
10	2177	T/T	T/T	T/T	T/C	T/T	T/T	T/T	T/T
11	5906	C/T	T/T	T/C	T/T	C/C	T/T	T/T	C/T
12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/T
13	8110	G/G	G/G	G/A	G/G	G/G	G/G	G/G	G/G
14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
15	8354	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
16	8402	A/A	A/A	A/A	A/G	A/A	A/A	A/A	A/A
17	8459	A/A	A/A	A/A	A/C	A/A	A/A	A/A	A/A
18	10203	G/G	G/G	G/G	G/G	G/G	G/A	G/G	G/G
19	10512	T/C	T/C	T/C	T/T	T/T	T/T	T/T	T/T

PS No.(a)	PS Position(b)	Haplotype Pair(c) (Part 3)							
		1/2	19/4	19/3	19/9	15/3	19/20	19/7	19/18
1	504	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
2	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
3	744	G/G	G/G	G/G	G/G	G/G	G/T	G/G	G/G
4	778	C/C	T/C	T/C	T/T	T/C	T/T	T/C	T/T
5	1009	C/C	G/G	G/G	G/C	G/G	G/G	G/G	G/G
6	1045	C/C	C/T	C/T	C/C	C/T	C/C	C/T	C/C
7	1122	G/G	G/G	G/A	G/G	G/A	G/G	G/G	G/G
8	1218	C/C	C/C	C/C	C/A	A/C	C/C	C/C	C/C
9	2014	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C
10	2177	T/T	T/T	T/T	T/T	T/T	T/T	T/C	T/T
11	5906	C/T	T/C	T/T	T/T	T/T	T/T	T/T	T/T
12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C
13	8110	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C
15	8354	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
16	8402	A/A	A/A	A/A	A/A	A/A	A/A	A/G	A/A
17	8459	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
18	10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
19	10512	T/T	T/T	T/C	T/T	T/C	T/T	T/T	T/C

PS No.(a)	PS Position(b)	Haplotype Pair(c) (Part 4) 22/17	19/12	1/12	19/8	15/10	19/15	19/10	18/16
1	504	T/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
2	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
4	778	T/T	T/T	C/T	T/T	T/T	T/T	T/T	T/T
5	1009	G/G	G/C	C/C	G/C	G/C	G/G	G/C	G/G
6	1045	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
8	1218	C/C	C/C	C/C	C/A	A/C	C/A	C/C	C/C
9	2014	C/C	C/T	C/T	C/C	C/C	C/C	C/C	C/C
10	2177	T/T	T/C	T/C	T/T	T/T	T/T	T/T	T/T
11	5906	T/T	T/T	C/T	T/C	T/C	T/T	T/C	T/C
12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
13	8110	A/A	G/G	G/G	G/G	G/G	G/G	G/G	G/G
14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
15	8354	A/A	A/A	A/A	A/G	A/A	A/A	A/A	A/A
16	8402	A/A	A/G	A/G	A/A	A/A	A/A	A/A	A/A
17	8459	A/A	A/C	A/C	A/A	A/A	A/A	A/A	A/A
18	10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
19	10512	C/T	T/T	T/T	T/T	T/T	T/T	T/T	C/T

PS No.(a)	PS Position(b)	Haplotype Pair(c) (Part 5) 3/14
1	504	G/G
2	717	C/C
3	744	G/G
4	778	C/T
5	1009	G/G
6	1045	T/C
7	1122	A/G
8	1218	C/A
9	2014	C/C
10	2177	T/T
11	5906	T/T
12	6010	C/C
13	8110	G/G
14	8333	C/C
15	8354	A/A
16	8402	A/A
17	8459	A/A
18	10203	G/G
19	10512	C/C

(a) PS = polymorphic site;
(b) Position of PS in SEQ ID NO:1;
(c) Haplotype pairs are represented as 1st haplotype/2nd haplotype; with alleles of each haplotype shown 5′ to 3′ as 1st polymorphism/2nd polymorphism in each column.

10. The method of claim 9, wherein the identified genotype of the individual comprises the nucleotide pair at each of PS1-PS19, which have the position and alternative alleles shown in SEQ ID NO:1.

11. A method for identifying an association between a trait and at least one haplotype or haplotype

pair of the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) gene which comprises comparing the frequency of the haplotype or haplotype pair in a population exhibiting the trait with the frequency of the haplotype or haplotype pair in a reference population, wherein the haplotype is selected from haplotypes 1-22 shown in the table presented immediately below, wherein each of the haplotypes comprises a sequence of polymorphisms whose positions and identities are set forth in the table immediately below:

PS No.(a)	PS Position(b)	Haplotype Number(c) (Part 1) 1	2	3	4	5	6	7	8	9	10
1	504	G	G	G	G	G	G	G	G	G	G
2	717	C	C	C	C	C	C	C	C	C	C
3	744	G	G	G	G	G	G	G	G	G	G
4	778	C	C	C	C	C	C	C	T	T	T
5	1009	C	C	G	G	G	G	G	C	C	C
6	1045	C	C	T	T	T	T	T	C	C	C
7	1122	G	G	A	G	G	G	G	G	G	G
8	1218	C	C	C	C	C	C	C	A	A	C
9	2014	C	C	C	C	C	C	T	C	C	C
10	2177	T	T	T	T	T	T	C	T	T	T
11	5906	C	T	T	C	T	T	T	C	T	C
12	6010	C	C	C	C	C	T	T	C	C	C
13	8110	G	G	G	G	G	G	G	G	G	G
14	8333	C	C	C	C	C	C	T	C	C	C
15	8354	A	A	A	A	A	A	A	G	A	A
16	8402	A	A	A	A	A	A	G	A	A	A
17	8459	A	A	A	A	A	A	A	A	A	A
18	10203	G	G	G	G	G	G	G	G	G	G
19	10512	T	T	C	T	T	T	T	T	T	T

PS No.(a)	PS Position(b)	Haplotype Number(c) (Part 2) 11	12	13	14	15	16	17	18	19	20
1	504	G	G	G	G	G	G	G	G	G	G
2	717	C	C	C	C	C	C	C	C	C	C
3	744	G	G	G	G	G	G	G	G	G	T
4	778	T	T	T	T	T	T	T	T	T	T
5	1009	C	C	G	G	G	G	G	G	G	G
6	1045	C	C	C	C	C	C	C	C	C	C
7	1122	G	G	G	G	G	G	G	G	G	G
8	1218	C	C	A	A	A	C	C	C	C	C
9	2014	C	T	C	C	C	C	C	C	C	C
10	2177	T	C	T	T	T	T	T	T	T	T
11	5906	T	T	C	T	T	C	T	T	T	T
12	6010	C	C	C	C	C	C	C	C	C	C
13	8110	G	G	A	G	G	G	A	G	G	G
14	8333	C	C	C	C	C	C	C	C	C	C
15	8354	A	A	A	A	A	A	A	A	A	A
16	8402	A	G	A	A	A	A	A	A	A	A
17	8459	A	C	A	A	A	A	A	A	A	A
18	10203	A	G	G	G	G	G	G	G	G	G
19	10512	T	T	C	C	T	T	T	C	T	T

PS No.(a)	PS Position(b)	Haplotype Number(c) (Part 3) 21	22
1	504	G	T
2	717	T	C
3	744	G	G
4	778	C	T
5	1009	C	G
6	1045	C	C
7	1122	G	G
8	1218	C	C
9	2014	C	C
10	2177	T	T
11	5906	C	T
12	6010	C	C
13	8110	G	A
14	8333	C	C
15	8354	A	A
16	8402	A	A
17	8459	A	A
18	10203	G	G
19	10512	T	C

(a) PS = polymorphic site;
(b) Position of PS within SEQ ID NO:1;
(c) Alleles for haplotypes are presented 5′ to 3′ in each column;

and wherein the haplotype pair is selected from the haplotype pairs shown in the table immediately below, wherein each of the TNFRSF11B haplotype pairs consists of first and second haplotypes which comprise first and second sequences of polymorphisms whose positions in SEQ ID NO:1 and identities are set forth in the table immediately below:

PS No.(a)	PS Position(b)	Haplotype Pair(c) (Part 1) 1/1	15/15	19/19	6/6	12/12	19/16	10/2	1/5
1	504	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
2	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
4	778	C/C	T/T	T/T	C/C	T/T	T/T	T/C	C/C
5	1009	C/C	G/G	G/G	G/G	C/C	G/G	C/C	C/G
6	1045	C/C	C/C	C/C	T/T	C/C	C/C	C/C	C/T
7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
8	1218	C/C	A/A	C/C	C/C	C/C	C/C	C/C	C/C
9	2014	C/C	C/C	C/C	C/C	T/T	C/C	C/C	C/C
10	2177	T/T	T/T	T/T	T/T	C/C	T/T	T/T	T/T
11	5906	C/C	T/T	T/T	T/T	T/T	T/C	C/T	C/T
12	6010	C/C	C/C	C/C	T/T	C/C	C/C	C/C	C/C
13	8110	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
15	8354	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
16	8402	A/A	A/A	A/A	A/A	G/G	A/A	A/A	A/A
17	8459	A/A	A/A	A/A	A/A	C/C	A/A	A/A	A/A
18	10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
19	10512	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T

PS No.(a)	PS Position(b)	Haplotype Pair(c) (Part 2) 10/14	19/14	19/13	15/12	1/21	19/11	15/6	1/6
1	504	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
2	717	C/C	C/C	C/C	C/C	C/T	C/C	C/C	C/C
3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
4	778	T/T	T/T	T/T	T/T	C/C	T/T	T/C	C/C
5	1009	C/G	G/G	G/G	G/C	C/C	G/C	G/G	C/G
6	1045	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/T
7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
8	1218	C/A	C/A	C/A	A/C	C/C	C/C	A/C	C/C
9	2014	C/C	C/C	C/C	C/T	C/C	C/C	C/C	C/C
10	2177	T/T	T/T	T/T	T/C	T/T	T/T	T/T	T/T
11	5906	C/T	T/T	T/C	T/T	C/C	T/T	T/T	C/T
12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/T
13	8110	G/G	G/G	G/A	G/G	G/G	G/G	G/G	G/G
14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
15	8354	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
16	8402	A/A	A/A	A/A	A/G	A/A	A/A	A/A	A/A
17	8459	A/A	A/A	A/A	A/C	A/A	A/A	A/A	A/A
18	10203	G/G	G/G	G/G	G/G	G/G	G/A	G/G	G/G
19	10512	T/C	T/C	T/C	T/T	T/T	T/T	T/T	T/T

PS No.(a)	PS Position(b)	Haplotype Pair(c) (Part 3) 1/2	19/4	19/3	19/9	15/3	19/20	19/7	19/18
1	504	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
2	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
3	744	G/G	G/G	G/G	G/G	G/G	G/T	G/G	G/G
4	778	C/C	T/C	T/C	T/T	T/C	T/T	T/C	T/T
5	1009	C/C	G/G	G/G	G/C	G/G	G/G	G/G	G/G
6	1045	C/C	C/T	C/T	C/C	C/T	C/C	C/T	C/C
7	1122	G/G	G/G	G/A	G/G	G/A	G/G	G/G	G/G
8	1218	C/C	C/C	C/C	C/A	A/C	C/C	C/C	C/C
9	2014	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C
10	2177	T/T	T/T	T/T	T/T	T/T	T/T	T/C	T/T
11	5906	C/T	T/C	T/T	T/T	T/T	T/T	T/T	T/T
12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C
13	8110	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C
15	8354	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
16	8402	A/A	A/A	A/A	A/A	A/A	A/A	A/G	A/A
17	8459	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
18	10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
19	10512	T/T	T/T	T/C	T/T	T/C	T/T	T/T	T/C

PS No.(a)	PS Position(b)	Haplotype Pair(c) (Part 4) 22/17	19/12	1/12	19/8	15/10	19/15	19/10	18/16
1	504	T/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
2	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
4	778	T/T	T/T	C/T	T/T	T/T	T/T	T/T	T/T
5	1009	G/G	G/C	C/C	G/C	G/C	G/G	G/C	G/G
6	1045	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
8	1218	C/C	C/C	C/C	C/A	A/C	C/A	C/C	C/C
9	2014	C/C	C/T	C/T	C/C	C/C	C/C	C/C	C/C
10	2177	T/T	T/C	T/C	T/T	T/T	T/T	T/T	T/T
11	5906	T/T	T/T	C/T	T/C	T/C	T/T	T/C	T/C
12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
13	8110	A/A	G/G	G/G	G/G	G/G	G/G	G/G	G/G
14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
15	8354	A/A	A/A	A/A	A/G	A/A	A/A	A/A	A/A
16	8402	A/A	A/G	A/G	A/A	A/A	A/A	A/A	A/A
17	8459	A/A	A/C	A/C	A/A	A/A	A/A	A/A	A/A
18	10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
19	10512	C/T	T/T	T/T	T/T	T/T	T/T	T/T	C/T

PS No.(a)	PS Position(b)	Haplotype Pair(c) (Part 5) 3/14
1	504	G/G
2	717	C/C
3	744	G/G
4	778	C/T
5	1009	G/G
6	1045	T/C
7	1122	A/G
8	1218	C/A
9	2014	C/C
10	2177	T/T
11	5906	T/T
12	6010	C/C
13	8110	G/G
14	8333	C/C
15	8354	A/A
16	8402	A/A
17	8459	A/A
18	10203	G/G
19	10512	C/C

(a) PS = polymorphic site;
(b) Position of PS in SEQ ID NO:1;
(c) Haplotype pairs are represented as 1st haplotype/2nd haplotype; with alleles of each haplotype shown 5′ to 3′ as 1st polymorphism/2nd polymorphism in each column;

wherein a higher frequency of the haplotype or haplotype pair in the trait population than in the reference population indicates the trait is associated with the haplotype or haplotype pair.

12. The method of claim 11, wherein the trait is a clinical response to a drug targeting TNFRSF11B or to a drug for treating a condition or disease predicted to be associated with TNFRSF11B

activity.

13. An isolated oligonucleotide designed for detecting a polymorphism in the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) gene at a polymorphic site (PS) selected from the group consisting of PS1, PS2, PS3, PS4, PS6, PS7, PS8, PS9, PS10, PS11, PS12, PS13, PS14, PS15, PS16, PS17, PS18 and PS19, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1.

14. The isolated oligonucleotide of claim 13, which is an allele-specific oligonucleotide that specifically hybridizes to an allele of the TNFRSF11B gene at a region containing the polymorphic site.

15. The allele-specific oligonucleotide of claim 14, which comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS:4-21, the complements of SEQ ID NOS:4-21, and SEQ ID NOS:22-57.

16. The isolated oligonucleotide of claim 13, which is a primer-extension oligonucleotide.

17. The primer-extension oligonucleotide of claim 16, which comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS:58-93.

18. A kit for haplotyping or genotyping the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) gene of an individual, which comprises a set of oligonucleotides designed to haplotype or genotype each of polymorphic sites (PS) PS1, PS2, PS3, PS4, PS6, PS7, PS8, PS9, PS10, PS11, PS12, PS13, PS14, PS15, PS16, PS17, PS18 and PS19, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1.

19. The kit of claim 18, which further comprises oligonucleotides designed to genotype or haplotype PS5, wherein the selected PS has the position and alternative alleles shown in SEQ ID NO:1.

20. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

    (a) a first nucleotide sequence which comprises a tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) isogene, wherein the TNFRSF11B isogene is selected from the group consisting of isogenes 1- 18 and 20 - 22 shown in the table immediately below and wherein each of the isogenes comprises the regions of SEQ ID NO:1 shown in the table immediately below and wherein each of the isogenes 1- 18 and 20 - 22 is further defined by the corresponding sequence of polymorphisms whose positions and identities are set forth in the table immediately below; and

Region Examined(a)	PS No.(b)	PS Position(c)	Isogene Number(d) (Part 1) 1	2	3	4	5	6	7	8	9	10
427-1437	1	504	G	G	G	G	G	G	G	G	G	G
427-1437	2	717	C	C	C	C	C	C	C	C	C	C
427-1437	3	744	G	G	G	G	G	G	G	G	G	G
427-1437	4	778	C	C	C	C	C	C	C	T	T	T
427-1437	5	1009	C	C	G	G	G	G	G	C	C	C
427-1437	6	1045	C	C	T	T	T	T	T	C	C	C
427-1437	7	1122	G	G	A	G	G	G	G	G	G	G
427-1437	8	1218	C	C	C	C	C	C	C	A	A	C
1604-2208	9	2014	C	C	C	C	C	C	T	C	C	C
1604-2208	10	2177	T	T	T	T	T	T	C	T	T	T
5748-6485	11	5906	C	T	T	C	T	T	T	C	T	C
5748-6485	12	6010	C	C	C	C	C	T	T	C	C	C
8035-8653	13	8110	G	G	G	G	G	G	G	G	G	G
8035-8653	14	8333	C	C	C	C	C	C	T	C	C	C
8035-8653	15	8354	A	A	A	A	A	A	A	G	A	A
8035-8653	16	8402	A	A	A	A	A	A	G	A	A	A
8035-8653	17	8459	A	A	A	A	A	A	A	A	A	A
9942-10628	18	10203	G	G	G	G	G	G	G	G	G	G
9942-10628	19	10512	T	T	C	T	T	T	T	T	T	T

Region Examined(a)	PS No.(b)	PS Position(c)	Isogene Number(d) (Part 2) 11	12	13	14	15	16	17	18	20
427-1437	1	504	G	G	G	G	G	G	G	G	G
427-1437	2	717	C	C	C	C	C	C	C	C	C
427-1437	3	744	G	G	G	G	G	G	G	G	T
427-1437	4	778	T	T	T	T	T	T	T	T	T
427-1437	5	1009	C	C	G	G	G	G	G	G	G
427-1437	6	1045	C	C	C	C	C	C	C	C	C
427-1437	7	1122	G	G	G	G	G	G	G	G	G
427-1437	8	1218	C	C	A	A	A	C	C	C	C
1604-2208	9	2014	C	T	C	C	C	C	C	C	C
1604-2208	10	2177	T	C	T	T	T	T	T	T	T
5748-6485	11	5906	T	T	C	T	T	C	T	T	T
5748-6485	12	6010	C	C	C	C	C	C	C	C	C
8035-8653	13	8110	G	G	A	G	G	G	A	G	G
8035-8653	14	8333	C	C	C	C	C	C	C	C	C
8035-8653	15	8354	A	A	A	A	A	A	A	A	A
8035-8653	16	8402	A	G	A	A	A	A	A	A	A
8035-8653	17	8459	A	C	A	A	A	A	A	A	A
9942-10628	18	10203	A	G	G	G	G	G	G	G	G
9942-10628	19	10512	T	T	C	C	T	T	T	C	T

Region Examined(a)	PS No.(b)	PS Position(c)	Isogene Number(d) (Part 3) 21	22
427-1437	1	504	G	T
427-1437	2	717	T	C
427-1437	3	744	G	G
427-1437	4	778	C	T
427-1437	5	1009	C	G
427-1437	6	1045	C	C
427-1437	7	1122	G	G
427-1437	8	1218	C	C
1604-2208	9	2014	C	C
1604-2208	10	2177	T	T
5748-6485	11	5906	C	T
5748-6485	12	6010	C	C
8035-8653	13	8110	G	A
8035-8653	14	8333	C	C
8035-8653	15	8354	A	A
8035-8653	16	8402	A	A
8035-8653	17	8459	A	A
9942-10628	18	10203	G	G
9942-10628	19	10512	T	C

(a) Region examined represents the nucleotide positions defining the start and stop positions within the 1st SEQ ID NO of the sequenced region;
(b) PS = polymorphic site;
(c) Position of PS in SEQ ID NO:1;
(d) Alleles for isogenes are presented 5′ to 3′ in each column;

(b) a second nucleotide sequence which is complementary to the first nucleotide sequence.

21. The isolated polynucleotide of claim 20, which is a DNA molecule and comprises both the first and second nucleotide sequences and further comprises expression regulatory elements operably linked to the first nucleotide sequence.

22. A recombinant nonhuman organism transformed or transfected with the isolated polynucleotide of claim 21, wherein the organism expresses a TNFRSF11B protein that is encoded by the first nucleotide sequence.

23. The recombinant nonhuman organism of claim 22, which is a transgenic animal.

24. An isolated fragment of a tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) isogene, wherein the fragment comprises at least 10 nucleotides in one of the regions of SEQ ID NO:1 shown in the table immediately below and wherein the fragment comprises one or more polymorphisms selected from the group consisting of thymine at PS1, thymine at PS2, thymine at PS3, cytosine at PS4, thymine at PS6, adenine at PS7, adenine at PS8, thymine at PS9, cytosine at PS10, cytosine at PS11, thymine at PS12, adenine at PS13, thymine at PS14, guanine at PS15, guanine at PS16, cytosine at PS17, adenine at PS18 and cytosine at PS19, wherein the selected polymorphism has the position set forth in the table immediately below:

Region Examined(a)	PS No.(b)	PS Position(c)	Isogene Number(d) (Part 1) 1	2	3	4	5	6	7	8	9	10
427-1437	1	504	G	G	G	G	G	G	G	G	G	G
427-1437	2	717	C	C	C	C	C	C	C	C	C	C
427-1437	3	744	G	G	G	G	G	G	G	G	G	G
427-1437	4	778	C	C	C	C	C	C	C	T	T	T
427-1437	5	1009	C	C	G	G	G	G	G	C	C	C
427-1437	6	1045	C	C	T	T	T	T	T	C	C	C
427-1437	7	1122	G	G	A	G	G	G	G	G	G	G
427-1437	8	1218	C	C	C	C	C	C	C	A	A	C
1604-2208	9	2014	C	C	C	C	C	C	T	C	C	C
1604-2208	10	2177	T	T	T	T	T	T	C	T	T	T
5748-6485	11	5906	C	T	T	C	T	T	T	C	T	C
5748-6485	12	6010	C	C	C	C	C	T	T	C	C	C
8035-8653	13	8110	G	G	G	G	G	G	G	G	G	G
8035-8653	14	8333	C	C	C	C	C	C	T	C	C	C
8035-8653	15	8354	A	A	A	A	A	A	A	G	A	A
8035-8653	16	8402	A	A	A	A	A	A	G	A	A	A
8035-8653	17	8459	A	A	A	A	A	A	A	A	A	A
9942-10628	18	10203	G	G	G	G	G	G	G	G	G	G
9942-10628	19	10512	T	T	C	T	T	T	T	T	T	T

Region Examined(a)	PS No.(b)	PS Position(c)	Isogene Number(d) (Part 2) 11	12	13	14	15	16	17	18	20
427-1437	1	504	G	G	G	G	G	G	G	G	G
427-1437	2	717	C	C	C	C	C	C	C	C	C
427-1437	3	744	G	G	G	G	G	G	G	G	T
427-1437	4	778	T	T	T	T	T	T	T	T	T
427-1437	5	1009	C	C	G	G	G	G	G	G	G
427-1437	6	1045	C	C	C	C	C	C	C	C	C
427-1437	7	1122	G	G	G	G	G	G	G	G	G
427-1437	8	1218	C	C	A	A	A	C	C	C	C
1604-2208	9	2014	C	T	C	C	C	C	C	C	C
1604-2208	10	2177	T	C	T	T	T	T	T	T	T
5748-6485	11	5906	T	T	C	T	T	C	T	T	T
5748-6485	12	6010	C	C	C	C	C	C	C	C	C
8035-8653	13	8110	G	G	A	G	G	G	A	G	G
8035-8653	14	8333	C	C	C	C	C	C	C	C	C
8035-8653	15	8354	A	A	A	A	A	A	A	A	A
8035-8653	16	8402	A	G	A	A	A	A	A	A	A
8035-8653	17	8459	A	C	A	A	A	A	A	A	A
9942-10628	18	10203	A	G	G	G	G	G	G	G	G
9942-10628	19	10512	T	T	C	C	T	T	T	C	T

Region Examined(a)	PS No.(b)	PS Position(c)	Isogene Number(d) (Part 3) 21	22
427-1437	1	504	G	T
427-1437	2	717	T	C
427-1437	3	744	G	G
427-1437	4	778	C	T
427-1437	5	1009	C	G
427-1437	6	1045	C	C
427-1437	7	1122	G	G
427-1437	8	1218	C	C
1604-2208	9	2014	C	C
1604-2208	10	2177	T	T
5748-6485	11	5906	C	T
5748-6485	12	6010	C	C
8035-8653	13	8110	G	A
8035-8653	14	8333	C	C
8035-8653	15	8354	A	A
8035-8653	16	8402	A	A
8035-8653	17	8459	A	A
9942-10628	18	10203	G	G
9942-10628	19	10512	T	C

(a) Region examined represents the nucleotide positions defining the start and stop positions within SEQ ID NO:1 of the regions sequenced;
(b) PS = polymorphic site;
(c) Position of PS within SEQ ID NO:1;
(d) Alleles for TNFRSF11B isogenes are presented 5′ to 3′ in each column.

25. An isolated polynucleotide comprising a coding sequence for a TNFRSF11B isogene, wherein the coding sequence comprises SEQ ID NO:2, except at each of the polymorphic sites which have the positions in SEQ ID NO:2 and polymorphisms set forth in the table immediately below:

PS No.(a)	PS Position(b)	Isogene Coding Sequence Number(c) (Part 1) 1c	2c	3c	7c	8c	9c	10c	11c	12c	13c
5	9	C	C	G	G	C	C	C	C	C	G
14	699	C	C	C	T	C	C	C	C	C	C
15	720	A	A	A	A	G	A	A	A	A	A
16	768	A	A	A	G	A	A	A	A	G	A
18	841	G	G	G	G	G	G	G	A	G	G
19	1150	T	T	C	T	T	T	T	T	T	C

PS No.(a)	PS Position(b)	Isogene Coding Sequence Number(c) (Part 2) 14c	18c	21c	22c
5	9	G	G	C	G
14	699	C	C	C	C
15	720	A	A	A	A
16	768	A	A	A	A
18	841	G	G	G	G
19	1150	C	C	T	C

(a) PS = polymorphic site;
(b) Position of PS in SEQ ID NO:2;
(c) Alleles for the isogene coding sequence are presented 5′ to 3′ in each column; the numerical

portion of the isogene coding sequence number represents the number of the parent full TNFRSF11B isogene.

26. A recombinant nonhuman organism transformed or transfected with the isolated polynucleotide of claim 25, wherein the organism expresses a tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) protein that is encoded by the polymorphic variant sequence.

27. The recombinant nonhuman organism of claim 26, which is a transgenic animal.

28. An isolated fragment of a TNFRSF11B coding sequence, wherein the fragment comprises one or more polymorphisms selected from the group consisting of thymine at a position corresponding to nucleotide 699, guanine at a position corresponding to nucleotide 720, guanine at a position corresponding to nucleotide 768, adenine at a position corresponding to nucleotide 841 and cytosine at a position corresponding to nucleotide 1150 in SEQ ID NO:2.

29 An isolated polypeptide comprising an amino acid sequence which is a polymorphic variant of a reference sequence for the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) protein, wherein the reference sequence comprises SEQ ID NO:3, except the polymorphic variant comprises one or more variant amino acids selected from the group consisting of methionine at a position corresponding to amino acid position 240 and methionine at a position corresponding to amino acid position 281.

30. An isolated monoclonal antibody specific for and immunoreactive with the isolated polypeptide of claim 29.

31. A method for screening for drugs targeting the isolated polypeptide of claim 29 which comprises contacting the TNFRSF11B polymorphic variant with a candidate agent and assaying for binding activity.

32. An isolated fragment of a TNFRSF11B protein, wherein the fragment comprises one or more variant amino acids selected from the group consisting of methionine at a position corresponding to amino acid position 240 and methionine at a position corresponding to amino acid position 281 in SEQ ID NO:3.

33. A computer system for storing and analyzing polymorphism data for the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) gene, comprising:

(a) a central processing unit (CPU);

(b) a communication interface;

(c) a display device;

(d) an input device; and

(e) a database containing the polymorphism data;

wherein the polymorphism data comprises the haplotypes set forth in the table immediately below:

PS No.(a)	PS Position(b)	Haplotype Number(c) (Part 1) 1	2	3	4	5	6	7	8	9	10
1	504	G	G	G	G	G	G	G	G	G	G
2	717	C	C	C	C	C	C	C	C	C	C
3	744	G	G	G	G	G	G	G	G	G	G
4	778	C	C	C	C	C	C	C	T	T	T
5	1009	C	C	G	G	G	G	G	C	C	C
6	1045	C	C	T	T	T	T	T	C	C	C
7	1122	G	G	A	G	G	G	G	G	G	G
8	1218	C	C	C	C	C	C	C	A	A	C
9	2014	C	C	C	C	C	C	T	C	C	C
10	2177	T	T	T	T	T	T	C	T	T	T
11	5906	C	T	T	C	T	T	T	C	T	C
12	6010	C	C	C	C	C	T	T	C	C	C
13	8110	G	G	G	G	G	G	G	G	G	G
14	8333	C	C	C	C	C	C	T	C	C	C
15	8354	A	A	A	A	A	A	A	G	A	A
16	8402	A	A	A	A	A	A	G	A	A	A
17	8459	A	A	A	A	A	A	A	A	A	A
18	10203	G	G	G	G	G	G	G	G	G	G
19	10512	T	T	C	T	T	T	T	T	T	T

PS No.(a)	PS Position(b)	Haplotype Number(c) (Part 2) 11	12	13	14	15	16	17	18	19	20
1	504	G	G	G	G	G	G	G	G	G	G
2	717	C	C	C	C	C	C	C	C	C	C
3	744	G	G	G	G	G	G	G	G	G	T
4	778	T	T	T	T	T	T	T	T	T	T
5	1009	C	C	G	G	G	G	G	G	G	G
6	1045	C	C	C	C	C	C	C	C	C	C
7	1122	G	G	G	G	G	G	G	G	G	G
8	1218	C	C	A	A	A	C	C	C	C	C
9	2014	C	T	C	C	C	C	C	C	C	C
10	2177	T	C	T	T	T	T	T	T	T	T
11	5906	T	T	C	T	T	C	T	T	T	T
12	6010	C	C	C	C	C	C	C	C	C	C
13	8110	G	G	A	G	G	G	A	G	G	G
14	8333	C	C	C	C	C	C	C	C	C	C
15	8354	A	A	A	A	A	A	A	A	A	A
16	8402	A	G	A	A	A	A	A	A	A	A
17	8459	A	C	A	A	A	A	A	A	A	A
18	10203	A	G	G	G	G	G	G	G	G	G
19	10512	T	T	C	C	T	T	T	C	T	T

PS No.(a)	PS Position(b)	Haplotype Number(c) (Part 3) 21	22
1	504	G	T
2	717	T	C
3	744	G	G
4	778	C	T
5	1009	C	G
6	1045	C	C
7	1122	G	G
8	1218	C	C
9	2014	C	C
10	2177	T	T
11	5906	C	T
12	6010	C	C
13	8110	G	A
14	8333	C	C
15	8354	A	A
16	8402	A	A
17	8459	A	A
18	10203	G	G
19	10512	T	C

(a) PS = polymorphic site;
(b) Position of PS within SEQ ID NO:1;
(c) Alleles for haplotypes are presented 5′ to 3′ in each column;

the haplotype pairs set forth in the table immediately below:

PS No.(a)	PS Position(b)	Haplotype Pair(c) (Part 1) 1/1	15/15	19/19	6/6	12/12	19/16	10/2	1/5
1	504	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
2	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
4	778	C/C	T/T	T/T	C/C	T/T	T/T	T/C	C/C
5	1009	C/C	G/G	G/G	G/G	C/C	G/G	C/C	C/G
6	1045	C/C	C/C	C/C	T/T	C/C	C/C	C/C	C/T
7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
8	1218	C/C	A/A	C/C	C/C	C/C	C/C	C/C	C/C
9	2014	C/C	C/C	C/C	C/C	T/T	C/C	C/C	C/C
10	2177	T/T	T/T	T/T	T/T	C/C	T/T	T/T	T/T
11	5906	C/C	T/T	T/T	T/T	T/T	T/C	C/T	C/T
12	6010	C/C	C/C	C/C	T/T	C/C	C/C	C/C	C/C
13	8110	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
15	8354	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
16	8402	A/A	A/A	A/A	A/A	G/G	A/A	A/A	A/A
17	8459	A/A	A/A	A/A	A/A	C/C	A/A	A/A	A/A
18	10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
19	10512	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T

	PS	PS	Haplotype Pair(c) (Part 2)							
	No.(a)	Position(b)	10/14	19/14	19/13	15/12	1/21	19/11	15/6	1/6
	1	504	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	2	717	C/C	C/C	C/C	C/C	C/T	C/C	C/C	C/C
	3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	4	778	T/T	T/T	T/T	T/T	C/C	T/T	T/C	C/C
	5	1009	C/G	G/G	G/G	G/C	C/C	G/C	G/G	C/G
	6	1045	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/T
	7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	8	1218	C/A	C/A	C/A	A/C	C/C	C/C	A/C	C/C
	9	2014	C/C	C/C	C/C	C/T	C/C	C/C	C/C	C/C
	10	2177	T/T	T/T	T/T	T/C	T/T	T/T	T/T	T/T
	11	5906	C/T	T/T	T/C	T/T	C/C	T/T	T/T	C/T
	12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/T
	13	8110	G/G	G/G	G/A	G/G	G/G	G/G	G/G	G/G
	14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	15	8354	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
	16	8402	A/A	A/A	A/A	A/G	A/A	A/A	A/A	A/A
	17	8459	A/A	A/A	A/A	A/C	A/A	A/A	A/A	A/A
	18	10203	G/G	G/G	G/G	G/G	G/G	G/A	G/G	G/G
	19	10512	T/C	T/C	T/C	T/T	T/T	T/T	T/T	T/T

	PS	PS	Haplotype Pair(c) (Part 3)							
	No.(a)	Position(b)	1/2	19/4	19/3	19/9	15/3	19/20	19/7	19/18
	1	504	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	2	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	3	744	G/G	G/G	G/G	G/G	G/G	G/T	G/G	G/G
	4	778	C/C	T/C	T/C	T/T	T/C	T/T	T/C	T/T
	5	1009	C/C	G/G	G/G	G/C	G/G	G/G	G/G	G/G
	6	1045	C/C	C/T	C/T	C/C	C/T	C/C	C/T	C/C
	7	1122	G/G	G/G	G/A	G/G	G/A	G/G	G/G	G/G
	8	1218	C/C	C/C	C/C	C/A	A/C	C/C	C/C	C/C
	9	2014	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C
	10	2177	T/T	T/T	T/T	T/T	T/T	T/T	T/C	T/T
	11	5906	C/T	T/C	T/T	T/T	T/T	T/T	T/T	T/T
	12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C
	13	8110	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C
	15	8354	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
	16	8402	A/A	A/A	A/A	A/A	A/A	A/A	A/G	A/A
	17	8459	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
	18	10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	19	10512	T/T	T/T	T/C	T/T	T/C	T/T	T/T	T/C

	PS No.(a)	PS Position(b)	Haplotype Pair(c) (Part 4) 22/17	19/12	1/12	19/8	15/10	19/15	19/10	18/16
150	1	504	T/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	2	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	4	778	T/T	T/T	C/T	T/T	T/T	T/T	T/T	T/T
	5	1009	G/G	G/C	C/C	G/C	G/C	G/G	G/C	G/G
155	6	1045	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	8	1218	C/C	C/C	C/C	C/A	A/C	C/A	C/C	C/C
	9	2014	C/C	C/T	C/T	C/C	C/C	C/C	C/C	C/C
	10	2177	T/T	T/C	T/C	T/T	T/T	T/T	T/T	T/T
160	11	5906	T/T	T/T	C/T	T/C	T/C	T/T	T/C	T/C
	12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	13	8110	A/A	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	15	8354	A/A	A/A	A/A	A/G	A/A	A/A	A/A	A/A
165	16	8402	A/A	A/G	A/G	A/A	A/A	A/A	A/A	A/A
	17	8459	A/A	A/C	A/C	A/A	A/A	A/A	A/A	A/A
	18	10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	19	10512	C/T	T/T	T/T	T/T	T/T	T/T	T/T	C/T

	PS No.(a)	PS Position(b)	Haplotype Pair(c) (Part 5) 3/14
170	1	504	G/G
	2	717	C/C
	3	744	G/G
175	4	778	C/T
	5	1009	G/G
	6	1045	T/C
	7	1122	A/G
	8	1218	C/A
180	9	2014	C/C
	10	2177	T/T
	11	5906	T/T
	12	6010	C/C
	13	8110	G/G
185	14	8333	C/C
	15	8354	A/A
	16	8402	A/A
	17	8459	A/A
	18	10203	G/G
190	19	10512	C/C

(a) PS = polymorphic site;
(b) Position of PS in SEQ ID NO:1;
(c) Haplotype pairs are represented as 1st haplotype/2nd haplotype; with alleles of each
195 haplotype shown 5′ to 3′ as 1st polymorphism/2nd polymorphism in each column;

or the frequency data in Tables 6 and 7.

34. A genome anthology for the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) gene which comprises two or more TNFRSF11B isogenes

selected from the group consisting of isogenes 1-22 shown in the table immediately below, and wherein each of the isogenes comprises the regions of SEQ ID NO:1 shown in the table immediately below and wherein each of the isogenes 1-22 is further defined by the corresponding sequence of polymorphisms whose positions and identities are set forth in the table immediately below:

Region Examined(a)	PS No.(b)	PS Position(c)	Isogene Number(d) (Part 1) 1	2	3	4	5	6	7	8	9	10
427-1437	1	504	G	G	G	G	G	G	G	G	G	G
427-1437	2	717	C	C	C	C	C	C	C	C	C	C
427-1437	3	744	G	G	G	G	G	G	G	G	G	G
427-1437	4	778	C	C	C	C	C	C	C	T	T	T
427-1437	5	1009	C	C	G	G	G	G	G	C	C	C
427-1437	6	1045	C	C	T	T	T	T	T	C	C	C
427-1437	7	1122	G	G	A	G	G	G	G	G	G	G
427-1437	8	1218	C	C	C	C	C	C	C	A	A	C
1604-2208	9	2014	C	C	C	C	C	C	T	C	C	C
1604-2208	10	2177	T	T	T	T	T	T	C	T	T	T
5748-6485	11	5906	C	T	T	C	T	T	T	C	T	C
5748-6485	12	6010	C	C	C	C	C	T	T	C	C	C
8035-8653	13	8110	G	G	G	G	G	G	G	G	G	G
8035-8653	14	8333	C	C	C	C	C	C	T	C	C	C
8035-8653	15	8354	A	A	A	A	A	A	A	G	A	A
8035-8653	16	8402	A	A	A	A	A	A	G	A	A	A
8035-8653	17	8459	A	A	A	A	A	A	A	A	A	A
9942-10628	18	10203	G	G	G	G	G	G	G	G	G	G
9942-10628	19	10512	T	T	C	T	T	T	T	T	T	T

Region Examined(a)	PS No.(b)	PS Position(c)	Isogene Number(d) (Part 2) 11	12	13	14	15	16	17	18	19	20
427-1437	1	504	G	G	G	G	G	G	G	G	G	G
427-1437	2	717	C	C	C	C	C	C	C	C	C	C
427-1437	3	744	G	G	G	G	G	G	G	G	G	T
427-1437	4	778	T	T	T	T	T	T	T	T	T	T
427-1437	5	1009	C	C	G	G	G	G	G	G	G	G
427-1437	6	1045	C	C	C	C	C	C	C	C	C	C
427-1437	7	1122	G	G	G	G	G	G	G	G	G	G
427-1437	8	1218	C	C	A	A	A	C	C	C	C	C
1604-2208	9	2014	C	T	C	C	C	C	C	C	C	C
1604-2208	10	2177	T	C	T	T	T	T	T	T	T	T
5748-6485	11	5906	T	T	C	T	T	C	T	T	T	T
5748-6485	12	6010	C	C	C	C	C	C	C	C	C	C
8035-8653	13	8110	G	G	A	G	G	G	A	G	G	G
8035-8653	14	8333	C	C	C	C	C	C	C	C	C	C
8035-8653	15	8354	A	A	A	A	A	A	A	A	A	A
8035-8653	16	8402	A	G	A	A	A	A	A	A	A	A
8035-8653	17	8459	A	C	A	A	A	A	A	A	A	A
9942-10628	18	10203	A	G	G	G	G	G	G	G	G	G
9942-10628	19	10512	T	T	C	C	T	T	T	C	T	T

Region Examined(a)	PS No.(b)	PS Position(c)	Isogene Number(d) (Part 3) 21	22
427-1437	1	504	G	T
427-1437	2	717	T	C
427-1437	3	744	G	G
427-1437	4	778	C	T
427-1437	5	1009	C	G
427-1437	6	1045	C	C
427-1437	7	1122	G	G
427-1437	8	1218	C	C
1604-2208	9	2014	C	C
1604-2208	10	2177	T	T
5748-6485	11	5906	C	T
5748-6485	12	6010	C	C
8035-8653	13	8110	G	A
8035-8653	14	8333	C	C
8035-8653	15	8354	A	A
8035-8653	16	8402	A	A
8035-8653	17	8459	A	A
9942-10628	18	10203	G	G
9942-10628	19	10512	T	C

(a) Region examined represents the nucleotide positions defining the start and stop positions within SEQ ID NO:1 of the regions sequenced;
(b) PS = polymorphic site;
(c) Position of PS within SEQ ID NO:1;
(d) Alleles for TNFRSF11B isogenes are presented 5′ to 3′ in each column.